

**Amendments to the Specification:**

In the paragraph under the title "CROSS-REFERENCE TO RELATED APPLICATION" on page 1 please replace the existing paragraph with the following amended paragraph (previously amended 9/5/03 by preliminary amendment):

This application is a continuation of U.S. Patent Application No. 09/713,426, filed November 15, 2000, which is a continuation-in-part of U.S. Patent Application No. 09/430,409, filed October 29, 1999, which is an application claiming benefit under 35 USC 119(e) of Application No. 60/121,453, filed February 24, 1999, ~~the disclosures of which are hereby specifically incorporated by reference.~~

Please replace the second full paragraph on page 8 with the following amended paragraph:

**Figure 4** shows a graphical comparison of gene representation in filtered maize libraries with random rice genomic clones. ~~(A) shows the proportions of exons and repeats in each library. (B) shows the proportion of low, medium and high copy sequences determined by hybridization.~~

Please replace the first full paragraph on page 18 with the following amended paragraph:

439 clones were end sequenced from the JM107MA2 maize library. For comparison, 340 randomly selected nonoverlapping bacterial artificial chromosome (BAC) end sequence reads from rice and 352 from Arabidopsis were downloaded from publicly available internet sites (~~e.g.,~~ <http://www.genome.clemson.edu/projects/rice.html>; <ftp://ftp.tigr.org/pub/data/a.thaliana/>). All of these sequences were subjected to sequence similarity searches.

Please replace the carryover paragraph between pages 18 and 19 with the following amended paragraph:

Similar maize libraries were constructed in the methylation restrictive *E. coli* host strains JM101, JM107 and JM109. The three strains were transformed with the same ligation mix used

to transform JM107MA2, and several hundred clones were end-sequenced from each library. BLASTN and BLASTX searches were performed against non-redundant nucleotide and protein sequence databases (GenBank-NCBI) and TBLASTX searches were performed against 'dbEST (GenBankNCBI) and 'at\_gb' ({Arabidopsis thaliana Genbank sequences collected by AtDb (~~http://genome~~[www.stanford.edu/Arabidopsis/dir.html](http://www.stanford.edu/Arabidopsis/dir.html); Flanders, D.J., et al. (1998) Nucleic Acids Res. 26:80)}).